

ABSTRACT OF THE DISCLOSURE

The invention relates to improved methods for directed evolution of polymers, including directed evolution of nucleic acids and proteins. Specifically, the methods of the invention include analytical methods for identifying "crossover locations" in a polymer. Crossovers at these locations are less likely to disrupt desirable properties of the protein, such as stability or functionality. The invention further provides improved methods for directed evolution wherein the polymer is selectively recombined at the identified "crossover locations". Crossover disruption profiles can be used to identify preferred crossover locations. Structural domains of a biopolymer can also be identified and analyzed, and domains can be organized into schema. Schema disruption profiles can be calculated, for example based on conformational energy or interatomic distances, and these can be used to identify preferred or candidate crossover locations. Computer systems for implementing analytical methods of the invention are also provided.

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